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RAW SEQUENCE LISTING

PATENT APPLICATION US/09/512,581

 DATE: 03/15/2000
 TIME: 13:43:08

Input Set: I512581.RAW

This Raw Listing contains the General Information
 Section and up to first 5 pages.

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1  <110> APPLICANT: Soto, Ana, et al.
2  <120> TITLE OF INVENTION: A NOVEL ANDROGEN-INDUCED SUPPRESSOR OF CELL PROLIFERATION
3  <130> FILE REFERENCE: MBI-008-1
4  <140> CURRENT APPLICATION NUMBER: US/09/512,581
5  <141> CURRENT FILING DATE: 2000-02-24
6  <160> NUMBER OF SEQ ID NOS: 5
7  <170> SOFTWARE: PatentIn Ver. 2.0
8  <210> SEQ ID NO 1
9  <211> LENGTH: 5271
10 <212> TYPE: DNA
11 <213> ORGANISM: Homo sapiens
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13 <221> NAME/KEY: CDS
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18      Met Ala His Ser Lys Thr Arg Thr Asn Asp Gly Lys Ile Thr Tyr
19      1          5          10          15
20      ccg cct ggg gtc aag gaa ata tca gat aaa ata tct aaa gag gag atg 158
21      Pro Pro Gly Val Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met
22      20          25          30
23      gtg aga cga tta aag atg gtt gtg aaa act ttt atg gat atg gac cag 206
24      Val Arg Arg Leu Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln
25      35          40          45
26      gac tct gaa gaa gaa aag gag ctt tat tta aac cta gct tta cat ctt 254
27      Asp Ser Glu Glu Glu Lys Glu Leu Tyr Leu Asn Leu Ala Leu His Leu
28      50          55          60
29      gct tca gat ttt ttt ctc aag cat cct ggt aaa gat gtt cgc tta ctg 302
30      Ala Ser Asp Phe Phe Leu Lys His Pro Gly Lys Asp Val Arg Leu Leu
31      65          70          75
32      gta gcc tgc tgc ctt gct gat att ttc agg att tat gct cct gaa gct 350
33      Val Ala Cys Cys Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala
34      80          85          90          95
35      cct tac aca tcc cct gat aaa cta aag gat ata ttt atg ttt ata aca 398
36      Pro Tyr Thr Ser Pro Asp Lys Leu Lys Asp Ile Phe Met Phe Ile Thr
37      100          105          110
38      aga cag ttg aag ggg cta gag gat aca aag agc cca caa ttc aat agg 446
39      Arg Gln Leu Lys Gly Leu Glu Asp Thr Lys Ser Pro Gln Phe Asn Arg
40      115          120          125
41      tat ttt tat tta ctt gag aac att gct tgg gtc aag tca tat aac ata 494
42      Tyr Phe Tyr Leu Leu Glu Asn Ile Ala Trp Val Lys Ser Tyr Asn Ile
43      130          135          140
44      tgc ttt gag tta gaa gat agc aat gaa att ttc acc cag cta tac aga 542
  
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47	acc tta ttt tca gtt ata aac aat ggc cac aat cag aaa gtc cat atg	590
48	Thr Leu Phe Ser Val Ile Asn Asn Gly His Asn Gln Lys Val His Met	
49	160 165 170 175	
50	cac atg gta gac ctt atg agc tct att att tgt gaa ggt gat aca gtg	638
51	His Met Val Asp Leu Met Ser Ser Ile Ile Cys Glu Gly Asp Thr Val	
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54	Ser Gln Glu Leu Leu Asp Thr Val Leu Val Asn Leu Val Pro Ala His	
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56	aag aat tta aac aag caa gca tat gat ttg gca aag gct tta ctg aag	734
57	Lys Asn Leu Asn Lys Gln Ala Tyr Asp Leu Ala Lys Ala Leu Leu Lys	
58	210 215 220	
59	agg aca gct caa gct att gag cca tat att acc act ttt ttt aat cag	782
60	Arg Thr Ala Gln Ala Ile Glu Pro Tyr Ile Thr Thr Phe Phe Asn Gln	
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62	gtt ctg atg ctt ggg aaa aca tct atc agc gat ttg tca gag cat gtc	830
63	Val Leu Met Leu Gly Lys Thr Ser Ile Ser Asp Leu Ser Glu His Val	
64	240 245 250 255	
65	ttt gac tta att ttg gag ctc tac aat att gat agt cat ttg ctg ctc	878
66	Phe Asp Leu Ile Leu Glu Leu Tyr Asn Ile Asp Ser His Leu Leu Leu	
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68	tct gtt tta ccc cag ctt gaa ttt aaa tta aag agc aat gat aat gag	926
69	Ser Val Leu Pro Gln Leu Glu Phe Lys Leu Lys Ser Asn Asp Asn Glu	
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72	Glu Arg Leu Gln Val Val Lys Leu Leu Ala Lys Met Phe Gly Ala Lys	
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75	Asp Ser Glu Leu Ala Ser Gln Asn Lys Pro Leu Trp Gln Cys Tyr Leu	
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77	ggc agg ttt aat gat atc cat gta cca atc cgc ctg gaa tgt gtg aaa	1070
78	Gly Arg Phe Asn Asp Ile His Val Pro Ile Arg Leu Glu Cys Val Lys	
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80	ttt gct agc cat tgt ctc atg aac cat cct gat tta gca aaa gac tta	1118
81	Phe Ala Ser His Cys Leu Met Asn His Pro Asp Leu Ala Lys Asp Leu	
82	340 345 350	
83	aca gag tat ctt aaa gtg agg tca cat gac cct gag gaa gct att aga	1166
84	Thr Glu Tyr Leu Lys Val Arg Ser His Asp Pro Glu Glu Ala Ile Arg	
85	355 360 365	
86	cat gat gtt att gtg tca ata gtt aca gct gct aaa aag gat att ctt	1214
87	His Asp Val Ile Val Ser Ile Val Thr Ala Ala Lys Lys Asp Ile Leu	
88	370 375 380	
89	ctg gtc aat gat cac tta ctt aat ttt gtg aga gag aga aca tta gac	1262
90	Leu Val Asn Asp His Leu Leu Asn Phe Val Arg Glu Arg Thr Leu Asp	
91	385 390 395	
92	aaa cga tgg aga gta cgc aaa gaa gcc atg atg gga ctt gcc caa att	1310
93	Lys Arg Trp Arg Val Arg Lys Glu Ala Met Met Gly Leu Ala Gln Ile	
94	400 405 410 415	

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96	Tyr Lys Lys Tyr Ala Leu Gln Ser Ala Ala Gly Lys Asp Ala Ala Lys	
97	420 425 430	
98	cag ata gca tgg atc aaa gac aaa ttg cta cat ata tat tat caa aat	1406
99	Gln Ile Ala Trp Ile Lys Asp Lys Leu Leu His Ile Tyr Tyr Gln Asn	
100	435 440 445	
101	agt att gat gat cga cta ctt gtt gaa cgg atc ttt gct caa tac atg	1454
102	Ser Ile Asp Asp Arg Leu Leu Val Glu Arg Ile Phe Ala Gln Tyr Met	
103	450 455 460	
104	gtt cct cac aat tta gaa act aca gaa cgg atg aaa tgc tta tat tac	1502
105	Val Pro His Asn Leu Glu Thr Thr Glu Arg Met Lys Cys Leu Tyr Tyr	
106	465 470 475	
107	ttg tat gcc aca ctg gat tta aat gct gtg aaa gca ttg aat gaa atg	1550
108	Leu Tyr Ala Thr Leu Asp Leu Asn Ala Val Lys Ala Leu Asn Glu Met	
109	480 485 490 495	
110	ttg aaa tgt caa aat ctg ctc cga cat caa gta aag gat ttg ctt gac	1598
111	Trp Lys Cys Gln Asn Leu Leu Arg His Gln Val Lys Asp Leu Leu Asp	
112	500 505 510	
113	ttg att aag caa ccc aaa aca gat gcc agt gtc aag gcc ata ttt tca	1646
114	Leu Ile Lys Gln Pro Lys Thr Asp Ala Ser Val Lys Ala Ile Phe Ser	
115	515 520 525	
116	aaa gtg atg gtt att aca aga aat tta cct gat cct ggt aag gct cag	1694
117	Lys Val Met Val Ile Thr Arg Asn Leu Pro Asp Pro Gly Lys Ala Gln	
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122	aga aag cag tta gaa gta ctt gtt agt cca aca tgc tcc tgc aag cag	1790
123	Arg Lys Gln Leu Glu Val Leu Val Ser Pro Thr Cys Ser Cys Lys Gln	
124	560 565 570 575	
125	gct gaa ggt tgt gtg cgt gaa ata act aag aag ttg ggc aac ccc aaa	1838
126	Ala Glu Gly Cys Val Arg Glu Ile Thr Lys Lys Leu Gly Asn Pro Lys	
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128	cag cct aca aat cct ttc ctg gaa atg atc aag ttt ctc ttg gag agg	1886
129	Gln Pro Thr Asn Pro Phe Leu Glu Met Ile Lys Phe Leu Leu Glu Arg	
130	595 600 605	
131	ata gca cct gtg cac ata gat acc gaa tct atc agt gct ctt att aaa	1934
132	Ile Ala Pro Val His Ile Asp Thr Glu Ser Ile Ser Ala Leu Ile Lys	
133	610 615 620	
134	caa gtg aac aaa tca ata gat gga aca gca gat gat gaa gat gag ggt	1982
135	Gln Val Asn Lys Ser Ile Asp Gly Thr Ala Asp Asp Glu Asp Glu Gly	
136	625 630 635	
137	gtt cca act gat caa gcc atc aga gca ggt ctt gaa ctg ctt aag gta	2030
138	Val Pro Thr Asp Gln Ala Ile Arg Ala Gly Leu Glu Leu Leu Lys Val	
139	640 645 650 655	
140	ctc tca ttt aca cat ccc atc tca ttt cat tct gct gaa aca ttt gaa	2078
141	Leu Ser Phe Thr His Pro Ile Ser Phe His Ser Ala Glu Thr Phe Glu	
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149	cca	cac	atc	aga	tca	gcc	ttg	ctt	cct	gtt	tta	cat	cac	aaa	tct	aaa		2222	
150	Pro	His	Ile	Arg	Ser	Ala	Leu	Leu	Pro	Val	Leu	His	His	Lys	Ser	Lys			
151					705				710					715					
152	aaa	gga	ccc	ccc	cgt	caa	gcc	aaa	tat	gcc	att	cat	tgt	atc	cat	gcg		2270	
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155	ata	ttt	tct	agt	aaa	gag	acc	cag	ttt	gca	cag	ata	ttt	gag	cct	ctg		2318	
156	Ile	Phe	Ser	Ser	Lys	Glu	Thr	Gln	Phe	Ala	Gln	Ile	Phe	Glu	Pro	Leu			
157					740					745						750			
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161	gtt	act	att	ggg	cat	att	gct	ctc	ctt	gca	cct	gat	caa	ttt	gct	gct		2414	
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164	cct	tgg	aaa	tct	tgg	gta	gct	act	ttc	att	gtg	aaa	gat	ctt	ctc	atg		2462	
165	Pro	Trp	Lys	Ser	Trp	Val	Ala	Thr	Phe	Ile	Val	Lys	Asp	Leu	Leu	Met			
166					785											795			
167	aat	gat	cgg	ctt	cca	ggg	aaa	aag	aca	act	aaa	ctt	tgg	gtt	cca	gat		2510	
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169																815			
170	gaa	gaa	gta	tct	cct	gag	aca	atg	gtc	aaa	att	cag	gct	att	aaa	atg		2558	
171	Glu	Glu	Val	Ser	Pro	Glu	Thr	Met	Val	Lys	Ile	Gln	Ala	Ile	Lys	Met			
172																830			
173	atg	gtt	cga	tgg	cta	ctt	gga	atg	aaa	aat	aat	cac	agt	aaa	tca	gga		2606	
174	Met	Val	Arg	Trp	Leu	Leu	Gly	Met	Lys	Asn	Asn	His	Ser	Lys	Ser	Gly			
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200	cat gca gct gtt agt gaa aaa tta ttg tct ctt cta cca gag tat gtt	3038
201	His Ala Ala Val Ser Glu Lys Leu Leu Ser Leu Leu Pro Glu Tyr Val	
202	980 985 990	
203	gtt cca tat aca att cac ctt ttg gca cat gac cca gat tat gtc aaa	3086
204	Val Pro Tyr Thr Ile His Leu Leu Ala His Asp Pro Asp Tyr Val Lys	
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206	gta cag gat att gaa caa ctt aaa gat gtt aaa gaa tgt ctt tgg ttt	3134
207	Val Gln Asp Ile Glu Gln Leu Lys Asp Val Lys Glu Cys Leu Trp Phe	
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209	gtt ctg gaa ata tta atg gct aaa aat gaa aat aac agt cac gct ttt	3182
210	Val Leu Glu Ile Leu Met Ala Lys Asn Glu Asn Asn Ser His Ala Phe	
211	1025 1030 1035	
212	atc aga aag atg gta gaa aat att aaa caa aca aaa gat gcc caa gga	3230
213	Ile Arg Lys Met Val Glu Asn Ile Lys Gln Thr Lys Asp Ala Gln Gly	
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215	cca gat gat gca aaa atg aat gaa aaa ctg tac act gtg tgt gat gtt	3278
216	Pro Asp Asp Ala Lys Met Asn Glu Lys Leu Tyr Thr Val Cys Asp Val	
217	1060 1065 1070	
218	gcc atg aat atc atc atg tca aag agt act aca tac agt ttg gaa tct	3326
219	Ala Met Asn Ile Ile Met Ser Lys Ser Thr Thr Tyr Ser Leu Glu Ser	
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221	cct aaa gac ccg gta cta cca gct cgt ttc ttc act caa cct gac aag	3374
222	Pro Lys Asp Pro Val Leu Pro Ala Arg Phe Phe Thr Gln Pro Asp Lys	
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224	aat ttc agt aac acc aaa aat tat ctg cct cct gaa atg aaa tca ttt	3422
225	Asn Phe Ser Asn Thr Lys Asn Tyr Leu Pro Pro Glu Met Lys Ser Phe	
226	1105 1110 1115	
227	ttc act cct gga aaa cct aaa aca acc aat gtt cta gga gct gtt aac	3470
228	Phe Thr Pro Gly Lys Pro Lys Thr Thr Asn Val Leu Gly Ala Val Asn	
229	1120 1125 1130 1135	
230	aag cca ctt tca tca gca ggc aag caa tct cag acc aaa tca tca cga	3518
231	Lys Pro Leu Ser Ser Ala Gly Lys Gln Ser Gln Thr Lys Ser Ser Arg	
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237	Gly Arg Ile Lys Gly Arg Leu Asp Ser Ser Glu Met Asp His Ser Glu	
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239	aat gaa gat tac aca atg tct tca cct ttg ccg ggg aaa aaa agt gac	3662
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